

SEQUENCE LISTING

<110> BUTZKE, DANIEL
 GOEDERT, SIGRID
 DITTRICH, MICHAEL
 RUDEL, THOMAS
 MEYER, THOMAS

<120> L-AMINO ACID OXIDASE WITH CYTOTOXIC ACTIVITY FROM
 APLYSIA PUNCTATA

<130> WEICKM-0046

<140> 10/542,769

<141> 2005-07-20

<150> PCT/EP04/00423

<151> 2004-01-20

<150> EP 03001232.2

<151> 2003-01-20

<150> EP 03026613.4

<151> 2003-11-19

<160> 78

<170> PatentIn Ver. 3.3

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<222> (1)..(1608)

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tgc ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga	144
Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly	
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gct aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg	192
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Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu	
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Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile	
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Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu	
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1608

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 Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
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 Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
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 Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
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 Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
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 Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
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 Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
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 Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
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 Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
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 Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
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 Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
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 385 390 395 400
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 Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
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 Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
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 Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
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 Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
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 Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
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 Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
 115 120 125
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 Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
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 Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
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 Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
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Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser	
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Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu	
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Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly	
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Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser	
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Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser	
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Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr	
275 280 285	
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Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly	
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Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp	
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Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp	
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Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile	
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 cag gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag 1344
 Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
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 Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
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 tca ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga 1536
 Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
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 ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tca gaa aac gtc 1584
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 <213> *Aplysia punctata*

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 Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
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 Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
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 Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu
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 Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly
 225 230 235 240
 Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser
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 Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser
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 Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly
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 Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp
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 Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe
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 385 390 395 400

Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu
 405 410 415

Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn
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Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
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 450 455 460

Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp
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Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
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Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
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 Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
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 Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
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 Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
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 Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
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Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro	
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Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr	
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Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val	
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Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg	
290 295 300	

gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat	960
Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn	
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Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro	
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Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu	
370 375 380	
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Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala	
420 425 430	
tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtg acc gcc gct tcc	1344
Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser	
435 440 445	
cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg	1392
Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg	
450 455 460	
gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca	1440
Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser	
465 470 475 480	
ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga ctt	1488
Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu	
485 490 495	
atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc	1536
Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile	
500 505 510	
aac gac tac ttc ctc taa	1554
Asn Asp Tyr Phe Leu	
515	

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Ser	Thr	Tyr	Asp	Val	Ala	Val	Val	Gly	Ala	Gly	Pro	Gly	Gly	Ala	Asn		
			20					25					30				
Ser	Ala	Tyr	Met	Leu	Arg	Asp	Ser	Gly	Leu	Asp	Ile	Ala	Val	Phe	Glu		
		35					40					45					
Tyr	Ser	Asp	Arg	Val	Gly	Gly	Arg	Leu	Phe	Thr	Tyr	Gln	Leu	Pro	Asn		
	50					55					60						
Thr	Pro	Asp	Val	Asn	Leu	Glu	Ile	Gly	Gly	Met	Arg	Phe	Ile	Glu	Gly		
	65				70					75					80		
Ala	Met	His	Arg	Leu	Trp	Arg	Val	Ile	Ser	Glu	Leu	Gly	Leu	Thr	Pro		
				85					90					95			
Lys	Val	Phe	Lys	Glu	Gly	Phe	Gly	Lys	Glu	Gly	Arg	Gln	Arg	Phe	Tyr		
			100					105					110				
Leu	Arg	Gly	Gln	Ser	Leu	Thr	Lys	Lys	Gln	Val	Lys	Ser	Gly	Asp	Val		
		115					120					125					
Pro	Tyr	Asp	Leu	Ser	Pro	Glu	Glu	Lys	Glu	Asn	Gln	Gly	Asn	Leu	Val		
	130					135					140						
Glu	Tyr	Tyr	Leu	Glu	Lys	Leu	Thr	Gly	Leu	Lys	Leu	Asn	Gly	Gly	Pro		
	145				150					155					160		
Leu	Lys	Arg	Glu	Val	Ala	Leu	Lys	Leu	Thr	Val	Pro	Asp	Gly	Arg	Phe		
				165					170					175			
Leu	Tyr	Asp	Leu	Ser	Phe	Asp	Glu	Ala	Met	Asp	Leu	Val	Ala	Ser	Pro		
			180					185					190				
Glu	Gly	Lys	Glu	Phe	Thr	Arg	Asp	Thr	His	Val	Phe	Thr	Gly	Glu	Val		
		195					200					205					
Thr	Leu	Asp	Ala	Ser	Ala	Val	Ser	Leu	Phe	Asp	Asp	His	Leu	Gly	Glu		
	210					215					220						
Asp	Tyr	Tyr	Gly	Ser	Glu	Ile	Tyr	Thr	Leu	Lys	Glu	Gly	Leu	Ser	Ser		
	225				230					235					240		
Val	Pro	Gln	Gly	Leu	Leu	Gln	Thr	Phe	Leu	Asp	Ala	Ala	Asp	Ser	Asn		
				245					250					255			
Glu	Phe	Tyr	Pro	Asn	Ser	His	Leu	Lys	Ala	Leu	Arg	Arg	Lys	Thr	Asn		
			260					265					270				

Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
 275 280 285
 Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg
 290 295 300
 Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn
 305 310 315 320
 Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro
 325 330 335
 Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
 340 345 350
 Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser
 355 360 365
 Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu
 370 375 380
 Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu
 385 390 395 400
 Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln
 405 410 415
 Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala
 420 425 430
 Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser
 435 440 445
 Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg
 450 455 460
 Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser
 465 470 475 480
 Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu
 485 490 495
 Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile
 500 505 510
 Asn Asp Tyr Phe Leu
 515

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 <212> DNA
 <213> Homo sapiens

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1 5 10 15	
gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct	96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser	
20 25 30	
gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc	144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe	
35 40 45	
acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa	192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu	
50 55 60	
gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct	240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser	
65 70 75 80	
cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga	288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly	
85 90 95	
ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att	336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile	
100 105 110	
gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg	384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg	
115 120 125	
ggc ctt ttt atc att gat gat aag ggt att ctt cgg cag atc act gta	432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val	
130 135 140	
aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt	480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val	
145 150 155 160	
cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc	528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	
165 170 175	
tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa	576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys	
180 185 190	
gaa tat ttc tcc aag cag aag tga	600
Glu Tyr Phe Ser Lys Gln Lys	
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 20 25 30
 Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
 35 40 45
 Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
 50 55 60
 Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
 65 70 75 80
 His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
 85 90 95
 Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
 100 105 110
 Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
 115 120 125
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
 130 135 140
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 145 150 155 160
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 165 170 175
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
 180 185 190
 Glu Tyr Phe Ser Lys Gln Lys
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<220>
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 Synthetic oligonucleotide

<220>
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 oligonucleotide

 <400> 9
 ggcugaugaa ggcaucucgt t 21

<210> 10
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
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 <400> 10
 augcuaaaau ugggcaccc 19

<210> 11
 <211> 19
 <212> RNA
 <213> Artificial Sequence

<220>
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 <400> 11
 ugcuaaaaau gggcacccu 19

<210> 12
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 <212> RNA
 <213> Artificial Sequence

<220>
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 <400> 12
 cuucaagcc acagcuguu 19

<210> 13
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 <212> RNA
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 <400> 13
 agccacagcu guuaugcca 19

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 <212> RNA
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<400> 14
 gccacagcug uuaugccag 19

<210> 15
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<400> 15
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<210> 16
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<210> 17
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<400> 17
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oligonucleotide

<400> 18

acucaacugc caagugauu

19

<210> 19

<211> 19

<212> RNA

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<400> 19

cucaacugcc aagugauug

19

<210> 20

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cugccaagug auuggugcu

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<400> 21

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<210> 23
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<400> 23
 caucccuug guaucagac 19

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<400> 24
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<400> 25
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<210> 26
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<400> 26
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<210> 27
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<400> 27
 accuggcagu gauaccauc 19

<210> 28
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<400> 28
 ccuggcagug auaccauca 19

<210> 29
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<400> 29
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 Synthetic oligonucleotide

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<400> 30
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<220>
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 Synthetic oligonucleotide

<220>
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<400> 31
 cuuacgcuga guacuucgat t

21

<210> 32
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 <213> Aplysia punctata

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 <223> Gln or Arg

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<400> 33
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 Phe Ala Asp Ser
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<210> 36
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 1 5

<210> 37
 <211> 15
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 <213> Aplysia punctata

<400> 37
 Ala Thr Cln Ala Tyr Ala Ala Val Arg Pro Ile Pro Ala Ser Lys
 1 5 10 15

Thr Gln Pro Ala Thr Thr Val Ala Ala Ala Glu Val Gln Cys Lys Lys
65 70 75 80

Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val
 85 90 95

Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro
 100 105 110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr
 115 120 125

Gly Tyr Gly Ser Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr
 130 135 140

Asn Pro Lys
 145

<210> 42

<211> 462

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 gttcaacgtg ganaagaaat tcgaagggtc cagaatcgtg agtttcaagc tcatccgcct 120
 gttcaacagg tncaagaagt gcaagaaagn ccagtattcc gtgtctggcg atgatgagga 180
 cncattcggt gtcagtgggt gttctggcgt gttccaggtn tgctacgaag aacaaacggc 240
 gcccgcctaca accnccacag aagccccgaa gccagagcca agaagacca agaggaaaaa 300
 tttcccaatc aaatttngta aacactgatg ggttaatntg acgaccagtg cgtctgcgaa 360
 agaatcatgt tatggttcat gatgtcatgc tcttaatat ggttgtaacg tttaacgcga 420
 tacagacatt aaaactcatt gttcaaaaaa aaaaaaaaaa aa 462

<210> 43
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 <213> Aplysia punctata

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 Ala Val Arg Xaa Val Gln Arg Gly Xaa Glu Ile Arg Arg Phe Gln Asn
 20 25 30

Arg	Glu	Phe	Gln	Ala	His	Pro	Pro	Val	Gln	Gln	Xaa	Gln	Glu	Val	Gln
		35					40					45			
Glu	Xaa	Pro	Val	Phe	Arg	Val	Trp	Arg	Xaa	Xaa	Gly	Xaa	Ile	Arg	Cys
	50					55					60				
Gln	Trp	Leu	Phe	Trp	Arg	Val	Pro	Gly	Xaa	Leu	Arg	Arg	Thr	Asn	Gly
65					70					75					80
Ala	Arg	Tyr	Asn	Xaa	His	Arg	Ser	Pro	Glu	Ala	Arg	Ala	Lys	Lys	Thr
				85					90					95	
Gln	Glu	Glu	Lys	Phe	Pro	Asn	Gln	Ile	Xaa	Xaa	Thr	Leu	Met	Gly	Xaa
			100					105					110		
Xaa	Asp	Asp	Gln	Cys	Val	Cys	Glu	Arg	Ile	Met	Leu	Trp	Phe	Met	Met
	115						120					125			
Ser	Cys	Ser	Xaa	Xaa	Tyr	Arg	Leu	Xaa	Arg	Leu	Thr	Arg	Tyr	Arg	His
	130					135					140				
Xaa	Asn	Ser	Leu	Phe	Lys	Lys	Lys	Lys	Lys	Lys					
145					150					155					

<210> 44
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 Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile
 20 25 30
 Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys
 35 40 45
 Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val
 50 55 60
 Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala
 65 70 75 80
 Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro
 85 90 95

Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn
 100 105 110

Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys
 115 120 125

His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys
 130 135 140

Thr His Cys Ser Lys Lys Lys Lys Lys
 145 150

<210> 45

<211> 153

<212> PRT

<213> *Aplysia punctata*

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<222> (6)..(7)

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 Cys Pro Xaa Gly Ser Thr Trp Xaa Arg Asn Ser Lys Val Pro Glu Ser
 20 25 30
 Xaa Val Ser Ser Ser Ser Ala Cys Ser Thr Gly Xaa Arg Ser Ala Arg
 35 40 45
 Lys Xaa Ser Ile Pro Cys Leu Ala Met Met Arg Xaa His Ser Leu Ser
 50 55 60
 Val Val Val Leu Ala Cys Ser Arg Xaa Ala Thr Lys Asn Lys Arg Arg
 65 70 75 80
 Pro Leu Gln Xaa Pro Gln Lys Pro Arg Ser Gln Ser Gln Glu Asp Pro
 85 90 95
 Arg Gly Lys Ile Ser Gln Ser Asn Xaa Val Asn Thr Asp Gly Leu Xaa
 100 105 110
 Xaa Arg Pro Val Arg Leu Arg Lys Asn His Val Met Val His Asp Val
 115 120 125
 Met Leu Leu Ile Xaa Val Val Thr Phe Asn Ala Ile Gln Thr Leu Lys
 130 135 140
 Leu Ile Val Gln Lys Lys Lys Lys Lys
 145 150

<210> 46
 <211> 9
 <212> PRT
 <213> Aplysia punctata

<220>
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 <222> (3)
 <223> Ile or Val

<400> 46
 Asp Gly Xaa Cys Arg Asn Arg Arg Gln
 1 5

<210> 47
 <211> 14
 <212> PRT
 <213> Aplysia punctata

<400> 47
 Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg
 1 5 10

<210> 48
 <211> 7
 <212> PRT
 <213> Aplysia punctata

<400> 48
 Val Phe Glu Tyr Ser Asp Arg
 1 5

<210> 49
 <211> 16
 <212> PRT
 <213> Aplysia punctata

<220>
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<400> 49
 Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile
 1 5 10 15

<210> 50
 <211> 10
 <212> PRT
 <213> Aplysia punctata

<400> 50
 Val Ile Scr Glu Leu Gly Leu Thr Pro Lys
 1 5 10

Thr Glu Pro Leu Lys
20

<210> 56
<211> 28
<212> PRT
<213> Aplysia punctata

<400> 56
Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn Ser Ala Tyr Met
1 5 10 15

Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
20 25

<210> 57
<211> 8
<212> PRT
<213> Aplysia punctata

<400> 57
Arg Val Gly Gly Arg Leu Phe Thr
1 5

<210> 58
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 58
tcctaacgta ggtctagacc tggtgcattt tttttttttt ttttt

45

<210> 59
<211> 22
<212> DNA
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<220>
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oligonucleotide

<220>
<221> modified_base
<222> {17}
<223> a, c, g, t, unknown or other

<400> 59
tcgtgttcga rtactengay cg

22

<210> 60
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 60
 ctgtaggtct agacctgttg ca 22

<210> 61
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 61
 ccgtgtagat ctactgccca ta 22

<210> 62
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 62
 ccgttgagtt gtagacct 18

<210> 63
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
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 oligonucleotide

<220>
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 <222> (24)
 <223> inosine

<220>
 <221> modified_base
 <222> (25)
 <223> inosine

<220>
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 <223> inosine

<220>
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 <222> (30)
 <223> inosine

<220>
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 <222> (34)
 <223> inosine

<220>
 <221> modified_base
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 <223> inosine

<400> 63
 ggccacgcgt cgactagtac gggnnngggnn gggnnng

36

<210> 64
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 64
 aattggccac gcgtcgacta gtac

24

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 65
 aattctcgtc tgctgtgctt ctcct

25

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 66
 gacttagagg aagtagtcgt tga 23

<210> 67
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 67
 ctggttatgcc agatggtcag 20

<210> 68
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 68
 gataccaaaag gaatgttcatt g 21

<210> 69
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 69
 caagaaggag ggtgacctga 20

<210> 70
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 70
 ttcgttgaag tcctactcta cg 22

<210> 71
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 71
 ggtatcgtgg aaggactcat gac 23

<210> 72
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 72
 gacttgccct tcgagtgacc gta 23

<210> 73
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic oligonucleotide

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 73
 cgagaugccu ucaucagcct t 21

<210> 74
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic oligonucleotide

<220>
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 oligonucleotide

<400> 74
 uguucuucug gaaguccagt t 21

<210> 75
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Combined DNA/RNA Molecule:
 Synthetic oligonucleotide

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 75
 ucgaaguacu cagcguaagt t

21

<210> 76
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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 consensus peptide

<220>
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 <222> (7)
 <223> variable amino acid

<220>
 <221> MOD_RES
 <222> (8)
 <223> Thr or Ser

<400> 76
 Arg His Gly Gly Arg His Xaa Xaa
 1 5

<210> 77
 <211> 13
 <212> PRT
 <213> Aplysia punctata

<220>
 <221> MOD_RES
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<400> 77
 Xaa Gly Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys
 1 5 10

<210> 78
 <211> 88
 <212> PRT
 <213> *Aplysia punctata*

<220>
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<220>
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 <223> variable amino acid

<220>
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 <222> (60)
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<220>
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 <222> (69)
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<220>
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 <222> (77)
 <223> variable amino acid

<400> 78
 Met Ser Ser Ala Val Leu Leu Leu Ala Cys Ala Leu Val Ile Ser Val
 1 5 10 15
 His Ala Asp Gly Xaa Xaa Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
 20 25 30
 Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
 35 40 45
 Ala Asn Ser Xaa Tyr Met Leu Arg Asp Ser Gly Xaa Asp Ile Ala Val
 50 55 60
 Phe Glu Tyr Ser Xaa Arg Val Gly Gly Arg Leu Phe Xaa Tyr Gln Leu
 65 70 75 80
 Pro Asn Thr Pro Asp Val Asn Leu
 85